

**\*09919854\***

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**ENTERED**

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/09/919,854

DATE: 01/16/2003

TIME: 13:51:17

Input Set : A:\211739USOX.ST25.txt

Output Set: N:\CRF4\01162003\I919854.raw

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3 <110> APPLICANT: FARWICK, MIKE
4   HUTHMACHER, KLAUS
5   BREHME, JENNIFER
6   PFEFFERLE, WALTER
7   BINDER, MICHAEL
8   GREISSINGER, DIETER
9   THIERBACH, GEORG
11 <120> TITLE OF INVENTION: Nucleotide sequences which code for the sahH gene
13 <130> FILE REFERENCE: 211739USOX
15 <140> CURRENT APPLICATION NUMBER: 09/919,854
C--> 16 <141> CURRENT FILING DATE: 2002-12-30
18 <150> PRIOR APPLICATION NUMBER: DE 100 44 706.6
19 <151> PRIOR FILING DATE: 2000-09-09
21 <150> PRIOR APPLICATION NUMBER: DE 101 09 685.2
22 <151> PRIOR FILING DATE: 2001-02-28
24 <150> PRIOR APPLICATION NUMBER: US 60/294,277
25 <151> PRIOR FILING DATE: 2001-05-31
27 <160> NUMBER OF SEQ ID NOS: 4
29 <170> SOFTWARE: PatentIn version 3.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 1939
33 <212> TYPE: DNA
34 <213> ORGANISM: Corynebacterium glutamicum
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (227)..(1720)
39 <223> OTHER INFORMATION:
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44 ttatccgcga actcgtcggg gagggctctg aagctcttcg cggtgctgca gcgcagggttt      120
46 tggaagaggc agatgtggaa tatgacctcg aagcttattt agaggccctc aactagccct      180
48 ccactaaaca gtttcaatca attcgggtgc cactccaaca tgtaga gtg gtg cgc      235
49                                     Val Val Arg
50                                     1
52 gtt aaa aaa gtt ttc cta att ttc att ttc tta aaa gga gct cgc cag      283
53 Val Lys Lys Val Phe Leu Ile Phe Ile Phe Leu Lys Gly Ala Arg Gln
54      5                      10                      15
56 gac atg gca cag gtt atg gac ttc aag gtt gcc gat ctt tca cta gca      331
57 Asp Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala
58 20                      25                      30                      35
60 gag gca gga cgt cac cag att cgt ctt gca gag tat gag atg cca ggt      379
61 Glu Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly
62                      40                      45                      50

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64 ctc atg cag ttg cgc aag gaa ttc gca gac gag cag cct ttg aag ggc 427
65 Leu Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly
66          55          60          65
68 gcc cga att gct ggt tct atc cac atg acg gtc cag acc gcc gtg ctt 475
69 Ala Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu
70          70          75          80
72 att gag acc ctc act gct ttg ggc gct gag gtt cgt tgg gct tcc tgc 523
73 Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys
74          85          90          95
76 aac att ttc tcc acc cag gat gag gct gca gcg gct atc gtt gtc ggc 571
77 Asn Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly
78 100          105          110          115
80 tcc gcc acc gtc gaa gag cca gct ggt gtt cca gta ttc gcg tgg aag 619
81 Ser Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys
82          120          125          130
84 ggt gag tca ctg gag gag tac tgg tgg tgc atc aac cag atc ttc agc 667
85 Gly Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser
86          135          140          145
88 tgg ggc gat gag ctg cca aac atg atc ctc gac gac ggc ggt gac gcc 715
89 Trp Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala
90          150          155          160
92 acc atg gct gtt att cgc ggt cgc gaa tac gag cag gct ggt ctg gtt 763
93 Thr Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val
94          165          170          175
96 cca cca gca gag gcc aac gat tcc gat gag tac atc gca ttc ttg ggc 811
97 Pro Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly
98 180          185          190          195
100 atg ctg cgt gag gtt ctt gct gca gag cct ggc aag tgg ggc aag atc 859
101 Met Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile
102          200          205          210
104 gct gag gcc gtt aag ggt gtc acc gag gaa acc acc acc ggt gtg cac 907
105 Ala Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His
106          215          220          225
108 cgc ctg tac cac ttc gct gaa gaa ggc gtg ctg cct ttc cca gcg atg 955
109 Arg Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met
110          230          235          240
112 aac gtc aac gac gct gtc acc aag tcc aag ttt gat aac aag tac ggc 1003
113 Asn Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly
114          245          250          255
116 acc cgc cac tcc ctg atc gac ggc atc aac cgc gcc act gac atg ctc 1051
117 Thr Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu
118 260          265          270          275
120 atg ggc ggc aag aac gtg ctt gtc tgc ggt tac ggc gat gtc ggc aag 1099
121 Met Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys
122          280          285          290
124 ggc tgc gct gag gct ttc gac ggc cag ggc gct cgc gtc aag gtc acc 1147
125 Gly Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr
126          295          300          305
128 gaa gct gac cca atc aac gct ctt cag gct ctg atg gat ggc tac tct 1195

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129 Glu Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser
130          310          315          320
132 gtg gtc acc gtt gat gag gcc atc gag gac gcc gac atc gtg atc acc 1243
133 Val Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr
134          325          330          335
136 gcg acc ggc aac aag gac atc att tcc ttc gag cag atg ctc aag atg 1291
137 Ala Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met
138 340          345          350          355
140 aag gat cac gct ctg ctg ggc aac atc ggt cac ttt gat aat gag atc 1339
141 Lys Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile
142          360          365          370
144 gat atg cat tcc ctg ttg cac cgc gac gac gtc acc cgc acc acg atc 1387
145 Asp Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile
146          375          380          385
148 aag cca cag gtc gac gag ttc acc ttc tcc acc ggt cgc tcc atc atc 1435
149 Lys Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile
150          390          395          400
152 gtc ctg tcc gaa ggt cgc ctg ttg aac ctt ggc aac gcc acc gga cac 1483
153 Val Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His
154          405          410          415
156 cca tca ttt gtc atg tcc aac tct ttc gcc gat cag acc att gcg cag 1531
157 Pro Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln
158 420          425          430          435
160 atc gaa ctg ttc caa aac gaa gga cag tac gag aac gag gtc tac cgt 1579
161 Ile Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg
162          440          445          450
164 ctg cct aag gtt ctc gac gaa aag gtg gca cgc atc cac gtt gag gct 1627
165 Leu Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala
166          455          460          465
168 ctc ggc ggt cag ctc acc gaa ctg acc aag gag cag gct gag tac atc 1675
169 Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile
170          470          475          480
172 ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac tac cgc tac 1720
173 Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr
174          485          490          495
176 taatgattgt cagcattgag ggaatcgacg gcgccggcaa aaacaccctg gtttcggcat 1780
178 taacgcaggt tattgatgca aaagtccttg cattcccacg ttatgaaacc tcgattcacg 1840
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182 ccatggccac gcttttcgcc ctgcaccgcc acttcgcga 1939
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186 <211> LENGTH: 498
187 <212> TYPE: PRT
188 <213> ORGANISM: Corynebacterium glutamicum
190 <400> SEQUENCE: 2
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193 1          5          10          15
196 Ala Arg Gln Asp Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu
197          20          25          30
200 Ser Leu Ala Glu Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu

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201	35	40	45
204 Met Pro Gly Leu Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro			
205 50	55	60	
208 Leu Lys Gly Ala Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr			
209 65	70	75	80
212 Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp			
213 85	90	95	
216 Ala Ser Cys Asn Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile			
217 100	105	110	
220 Val Val Gly Ser Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe			
221 115	120	125	
224 Ala Trp Lys Gly Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln			
225 130	135	140	
228 Ile Phe Ser Trp Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly			
229 145	150	155	160
232 Gly Asp Ala Thr Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala			
233 165	170	175	
236 Gly Leu Val Pro Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala			
237 180	185	190	
240 Phe Leu Gly Met Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp			
241 195	200	205	
244 Gly Lys Ile Ala Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr			
245 210	215	220	
248 Gly Val His Arg Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe			
249 225	230	235	240
252 Pro Ala Met Asn Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn			
253 245	250	255	
256 Lys Tyr Gly Thr Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr			
257 260	265	270	
260 Asp Met Leu Met Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp			
261 275	280	285	
264 Val Gly Lys Gly Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val			
265 290	295	300	
268 Lys Val Thr Glu Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp			
269 305	310	315	320
272 Gly Tyr Ser Val Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile			
273 325	330	335	
276 Val Ile Thr Ala Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met			
277 340	345	350	
280 Leu Lys Met Lys Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp			
281 355	360	365	
284 Asn Glu Ile Asp Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg			
285 370	375	380	
288 Thr Thr Ile Lys Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg			
289 385	390	395	400
292 Ser Ile Ile Val Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala			
293 405	410	415	
296 Thr Gly His Pro Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr			
297 420	425	430	

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300 Ile Ala Gln Ile Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu
301           435           440           445
304 Val Tyr Arg Leu Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His
305           450           455           460
308 Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala
309 465           470           475           480
312 Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr
313           485           490           495
316 Arg Tyr
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321 <211> LENGTH: 28
322 <212> TYPE: DNA
323 <213> ORGANISM: ARTIFICIAL SEQUENCE
325 <220> FEATURE:
326 <223> OTHER INFORMATION: SYNTHETIC DNA
328 <400> SEQUENCE: 3
329 gtggtacctt cgggtgtccac tccaacat                28
332 <210> SEQ ID NO: 4
333 <211> LENGTH: 28
334 <212> TYPE: DNA
335 <213> ORGANISM: ARTIFICIAL SEQUENCE
337 <220> FEATURE:
338 <223> OTHER INFORMATION: SYNTHETIC DNA
340 <400> SEQUENCE: 4
341 catctagata ggcgctgtcg gtgaggtc                28

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**VERIFICATION SUMMARY**

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Input Set : A:\211739US0X.ST25.txt

Output Set: N:\CRF4\01162003\I919854.raw

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L:41 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:39